SEQUENCE LISTING

<110>	Better, Marc Horwitz, Arn								
<120>	Human Engine	ered to	Antibo	dies to	Ep-CAM				
<130>	14923US02								
	60/459,334 2003-03-31								
<160>	59								
<170>	PatentIn ver	sion 3.2							
<210> <211> <212> <213>	720								
<220> <221> <223>	misc_feature Mouse Human		Light	Chain	DNA and	Protein			
<220> <221> <222>	CDS (1)(717)								
	mat_peptide (61)()								
<400>									4.0
	g ttc tct gct g Phe Ser Ala								48
	c act gca gat r Thr Ala Asp -1 1			hr Gln					96
	t ctt gga aca r Leu Gly Thr 15								144
	a cat agt aat u His Ser Asn			_		_	_	-	192
	c cag tct cct y Gln Ser Pro								240

tca gga gtc Ser Gly Val									_		288
aca ctg aga Thr Leu Arg				la Glu							336
tgt gct caa Cys Ala Gln 95											384
ctt gag atg Leu Glu Met 110					Ser						432
cca tct gat Pro Ser Asp 125											480
ctg aat aac Leu Asn Asn											528
aac gcc ctc Asn Ala Leu				ln Glu							576
agc aag gac Ser Lys Asp 175						_	_	-	-		624
gca gac tac Ala Asp Tyr 190					Cys						672
ggc ctg agc Gly Leu Ser 205										tag	720
	Sapiens										
<400> 2 Met Arg Phe	Ser Ala	Gln Leu	Leu Gl	ly Leu	Leu '	Val	Leu	Tro	Ile	Pro	
-20	302 1114	-15		., neu	-10			115	116	-5	

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro

			-1	1				5					10		
Val	Thr	Leu 15	Gly	Thr	Ser	Gly	Ser 20	Ile	Ser	Cys	Arg	Ser 25	Ser	Lys	Ser
Leu	Leu 30	His	Ser	Asn	Gly	Ile 35	Thr	Tyr	Leu	Tyr	Trp 40	Tyr	Leu	Gln	Lys
Pro 45	Gly	Gln	Ser	Pro	Gln 50	Leu	Leu	Ile	Tyr	Gln 55	Met	Ser	Asn	Leu	Ala 60
Ser	Gly	Val	Pro	Asp 65	Arg	Phe	Ser	Ser	Ser 70	Gly	Ser	Gly	Thr	Asp 75	Phe
Thr	Leu	Arg	Ile 80	Ser	Arg	Val	Glu	Ala 85	G1u	Asp	Val	Gly	Val 90	Tyr	Tyr
Cys	Ala	Gln 95	Asn	Leu	Glu	Leu	Pro 100	Arg	Thr	Phe	Gly	Gly 105	Gly	Thr	Lys
Leu	Glu 110	Met	Lys	Arg	Thr	Val 115	Ala	Ala	Pro	Ser	Val 120	Phe	Ile	Phe	Pro
Pro 125	Ser	Asp	Glu	Gln	Leu 130	Lys	Ser	Gly	Thr	Ala 135	Ser	Val	Val	Cys	Leu 140
Leu	Asn	Asn	Phe	Tyr 145	Pro	Arg	Glu	Ala	Lys 150	Val	Gln	Trp	Lys	Val 155	Asp
Asn	Ala	Leu	Gln 160	Ser	Gly	Asn	Ser	Gln 165	Glu	Ser	Val	Thr	Glu 170	Gln	Asp
Ser	Lys	Asp 175	Ser	Thr	Tyr	Ser	Leu 180	Ser	Ser	Thr	Leu	Thr 185	Leu	Ser	Lys
Ala	Asp 190	Tyr	Glu	Lys	His	Lys 195	Val	Tyr	Ala	Cys	Glu 200	Val	Thr	His	Gln
Gly 205	Leu	Ser	Ser	Pro	Val 210	Thr	Lys	Ser	Phe	Asn 215	Arg	Gly	Glu	Cys	

```
<210> 3
<211> 1398
<212> DNA
<213> Homo Sapiens
<220>
<221> misc_feature
       Mouse-Human chimeric Heavy Chain DNA and Protein Sequence
<220>
<221>
       CDS
<222>
       (1)..(1395)
<220>
<221>
       mat_peptide
<222>
       (58)..()
<400> 3
atg gct tgg gtg tcc acc ttg cta ttc ctg atg gca gct gcc caa agt
                                                                       48
Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                -15
                                    -10
gcc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag
                                                                       96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
        -1 1
cct gga gag aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc
                                                                      144
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
aca aaa tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta
                                                                      192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt
                                                                      240
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
                50
                                    55
gat gac ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc
                                                                      288
Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
            65
                                70
                                                     75
act gcc aat ttg cag atc aac aac ctc aaa agt gag gac acg gct aca
                                                                      336
Thr Ala Asn Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Thr Ala Thr
        80
tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga
                                                                      384
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
    95
                        100
acc tcg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc
                                                                      432
Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
```

110	115	120	125
		tct ggg ggc aca gcg Ser Gly Gly Thr Ala 135	
		gaa ccg gtg acg gtg Glu Pro Val Thr Val 155	
		cac acc ttc ccg gct His Thr Phe Pro Ala 170	
		agc gtg gtg acc gtg Ser Val Val Thr Val 185	
	_	tgc aac gtg aat cac Cys Asn Val Asn His 200	_
		gag ccc aaa tct tgt Glu Pro Lys Ser Cys 215	_
		cct gaa ctc ctg ggg Pro Glu Leu Leu Gly 235	
		aag gac acc ctc atg Lys Asp Thr Leu Met 250	
		gtg gac gtg agc cac Val Asp Val Ser His 265	
		gac ggc gtg gag gtg Asp Gly Val Glu Val 280	
		tac aac agc acg tac Tyr Asn Ser Thr Tyr 295	
		gac tgg ctg aat ggc Asp Trp Leu Asn Gly 315	
		ctc cca gcc ccc atc Leu Pro Ala Pro Ile 330	

				aaa Lys	 _	_	_		_				110	4
_				gat Asp 355	 -	_		_	-	_	_		115	2
				ttc Phe									120	0
_		 _	_	gag Glu		_		_				_	124	8
				ttc Phe									129	6
				Gly									134	4
				tac Tyr 435									139	2
aaa Lys	tga												139	8

<210> 4

<211> 465

<212> PRT.

<213> Homo Sapiens

<400> 4

Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
-15 -10 -5

Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys -1 1 5 10

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe 15 20 25

Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu 30 40 45

Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly 50 55 60

Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser 65 70 75

Thr Ala Asn Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Thr Ala Thr 80 85 90

Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly 95 100 105

Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe 110 125 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp 145 150 155

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu 160 165 170

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser 175 180 185

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro 190 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro 225 230 235

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser 240 245 250

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp 255

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn 270

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu 305 310 315

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys 320 325 330

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr 335 340 345

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr 350 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu 370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu 385 390 395

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys 400 405 410 \cdot

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu 415 420 425

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly 430 435 440 445

Lys

<210> 5 <211> 720

```
<212> DNA
<213> Homo Sapiens
<220>
<221>
      misc_feature
<223>
       Low Risk Human Engineered ING-1 Light Chain (LC)
<220>
<221> misc_feature
<223> Variable Region of the Light Chain is Amino Acids 1-112
<220>
<221> CDS
<222>
      (1)..(717)
<220>
<221> mat_peptide
<222>
      (61)..()
<400> 5
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct
                                                                       48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
gga tcc act gca gac atc gtg atg acc cag tct gca ctc tcc aat cca
                                                                       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
            -1 1
gtc act ctg gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt
                                                                      144
Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
        15
                            20
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg caq aaa
                                                                      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30
                        35
cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc
                                                                      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45
                    50
                                                             60
tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc
                                                                      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65
                                    70
act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac
                                                                      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag
                                                                      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg
                                                                      432
```

	Glu 110	Met	Lys	Arg	Thr	Val 115	Ala	Ala	Pro	Ser	Val 120	Phe	Ile	Phe	Pro	
cca Pro 125																480
ctg Leu																528
aac Asn																576
agc Ser								agc Ser								624
gca Ala																672
ggc Gly 205								agc Ser							tag	720
<210 <211 <212 <213	.> 2 !> I	5 239 PRT Homo	Sap:	iens												
<211 <212	.> 2 !> I !> I	239 PRT	Sap:	iens												
<211 <212 <213	> 2 > I > I	239 PRT Homo	_		Gln -15	Leu	Leu	Gly	Leu	Leu -10	Val	Leu	Trp	Ile	Pro	
<211 <212 <213 <400 Met -20	> 2 > I > I > F Arg	239 PRT Homo 5	Ser	Ala	-15			Gly Thr 5		-10			_		-5	
<211 <212 <213 <400 Met -20	> 2 > I > I > Arg	239 PRT Homo 5 Phe Thr	Ser Ala	Ala Asp 1	-15	Val	Met	Thr 5	Gln	-10 Ser	Ala	Ļeu	Ser 10	Asn	-5 Pro	
<211 <212 <213 <400 Met -20 Gly Val	> 2 > I > F > Arg	Phe Thr	Ser Ala -1	Ala Asp 1	-15 Ile Ser	Val Gly	Met Ser 20	Thr 5	Gln Ser	-10 Ser Cys	Ala Arg	Leu Ser 25	Ser 10	Asn Lys	-5 Pro Ser	

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe 65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr 80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys 95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro 110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu 125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp 145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp 160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys 175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
190 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 205 210 215

<210> 7

<211> 720

<212> DNA

<213> Homo Sapiens

<220>

<221> misc_feature

<223> Low + Moderate Risk Human Engineered ING-1 Light Chain (LC)

<220>

<221> CDS

<222> (1)..(717)

<220> <221> mat_peptide <222> (61)()			
<400> 7 atg agg ttc tct gct Met Arg Phe Ser Ala -20			
gga tcc act gca gad Gly Ser Thr Ala Asp -1 1		Gln Ser Pro Leu	
gtc act cct gga gag Val Thr Pro Gly Glu 15			
ctc cta cat agt aat Leu Leu His Ser Asr 30			
cca ggg cag tct cct Pro Gly Gln Ser Pro 45			
tca ggg gtc cca gad Ser Gly Val Pro Asp 65			
act ctc aag atc ago Thr Leu Lys Ile Ser 80		Glu Asp Val Gly	
tgt gct cag aac cta Cys Ala Gln Asn Leu 95			
ctt gag atg aaa cga Leu Glu Met Lys Arg 110			
cca tct gat gag cag Pro Ser Asp Glu Glr 125			
ctg aat aac ttc tat Leu Asn Asn Phe Tyr 145	r Pro Arg Glu Ala		
aac gcc ctc caa tcg Asn Ala Leu Gln Ser 160		Glu Ser Val Thr (

agc aag gac agc acc tac agc ctc agc acc ctg acg ctg agc aaa 6 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys 175 180 185	524
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 190 195 200	72
ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 215	20
<210> 8 <211> 239 <212> PRT <213> Homo Sapiens	
<400> 8	
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro -20 -15 -10 -5	
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro -1 1 5 10	
Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser 15 20 25	
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys 30 35 40	
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala 45 50 55 60	
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe 65 70 75	
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr 80 85 90	
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys 95 100 105	
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro 110 115 120	

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu 125 130 135 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp 145 150 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp 160 165 170 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys 175 180 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 195 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 210 <210> 9 <211> 88 <212> DNA <213> Homo Sapiens <220> <221> misc_feature <223> KL1 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low) <400> 9 tgtcgacacc atgaggttct ctgctcagct tctggggctg cttgtgctct ggatccctgg 60 atccactgca gacatcgtga tgacccag 88 <210> 10 <211> 85 <212> DNA <213> Homo Sapiens <220> <221> misc_feature <223> KL2 V Region Oligos Human Engineered ING-1 Light Chain (Kappa

<400>					
actctta	acta gaccggcagg agatggaacc	tgactctccc	agagtgactg	gattggagag	60
tgcagad	ctgg gtcatcacga tgtct				85
<210>	11				
<211>	88				
<212>	DNA				
<213>	Homo Sapiens				
<220>					
<221>	misc_feature				
<223>	KL3 V Region Oligos Human	Engineered	ING-1 Light	Chain (Kappa	
	low)				
<400>	11				
ctgccgg	gtct agtaagagtc tcctacatag	taatggcatc	acttatttgt	attggtatct	60
gcagaaa	acca gggcagtctc ctcagctg				88
<210>	12				
<211>	86				
<212>	DNA				
<213>	Homo Sapiens				
	*				
<220>					
<221>	misc_feature				
<223>	KL4 V Region Oligos Human	Engineered	ING-1 Light	Chain (Kappa	
	low)				
<400>	12				
tgtccca	agat ccactgctac tgaacctgtc	tgggacccct	gaggctctgt	tagacatctg	60
atagato	gage agetgaggag aetgee		• .		86
	J. J. 1911.J. J.				
<210>	13				
<211>	77				
<212>	DNA	•			
<213>	Homo Sapiens				
<220>					
<221>	misc_feature				
<223>	KL5 V Region Oligos Human	Engineered	ING-1 Light	Chain (Kappa	
	low)				
<400>	13				<u></u> .
agcagto	ggat ctgggacaga tttcactctc (aagatcagca	gagtggaggc	tgaagatgtg	60

ggagtt	tatt actgtgc	77
<210> <211> <212> <213>	14 75 DNA Homo Sapiens	
	<pre>misc_feature KL6 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)</pre>	
<400>	14	
tttgati	ttca agettggtge cetgaeegaa egteegtgga agetetaggt tetgageaea	60
gtaata	aact cccac	75
<210><211><211><212><213>	15 22 DNA Homo Sapiens	
<223>	misc_feature Low Risk Primers Forward Primer: KF ING-1 Light Chain Oligos	
<400>	15 cgac accatgaggt tc	22
_		
<210><211><211><212><213>	16 21 DNA Homo Sapiens	
<220> <221> <223>	misc_feature Low risk Primers Reverse Primer: KR ING-1 Light Chain Oligos	
<400>	16	
tttgati	ttca agcttggtgc c	21
<210><211><212><212><213>	17 85 DNA Homo Sapiens	

```
<220>
<221>
      misc_feature
      Moderate Risk Primer: KM2 V Region Oligos Human Engineered ING-1
<223>
       Light Chain Oligos (Kappa Moderate)
<400> 17
actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gcagggagag
                                                                       60
tggagactgg gtcatcacga tgtct
                                                                       85
<210> 18
<211>
      1398
<212>
      DNA
<213>
      Homo Sapiens
<220>
<221>
      misc_feature
<223>
      Low Risk Human Engineered ING-1 Heavy Chain (HC)
<220>
<221> misc_feature
<223>
      Variable region of HC is Amino Acids is 1-116
<220>
<221> CDS
<222>
       (1)..(1395)
<220>
<221> mat_peptide
<222>
      (58)..()
<400> 18
atg gct tgg gtg tcc acc ttg cta ttc ctg atg gca gct gcc caa agt
                                                                       48
Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
                -15
                                    -10
gcc caa gca cag atc cag ttg gtg cag tct gga cct gag gtg aag aag
                                                                       96
Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
        -1 1
cct gga gag tcc gtc aag atc tcc tgc aag gct tct gga tat acc ttc
                                                                      144
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    15
                        20
aca aaa tat gga atg aac tgg gtg aag cag gct cca gga cag ggt tta
                                                                      192
Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
30
                    35
                                                             45
aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt
                                                                      240
Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
                50
                                                        60
```

_	gac Asp													288
	gcc Ala		_	_					 _					336
	ttc Phe 95	_	_	_				_	 _					384
	ttg Leu	_		_			_	_	_		_	_		432
	ctg Leu													480
	tgc Cys													528
	tca Ser		_	_		_				_	-	~		576
	tcc Ser 175													624
	agc Ser													672
	aac Asn													720
	cac His		_		_	_		_	_	_			_	768
	gtc Val								_		_			816
	acc Thr 255													864
	gag Glu		_											912

270	275	280	285
	cgg gag gag cag tac Arg Glu Glu Gln Tyr 295	Asn Ser Thr Tyr Arg	y Val
	gtc ctg cac cag gac Val Leu His Gln Asp 310		
	tcc aac aaa gcc ctc Ser Asn Lys Ala Leu 325		•
	aaa ggg cag ccc cga Lys Gly Gln Pro Arg 340		
_	gat gag ctg acc aag Asp Glu Leu Thr Lys 355		
	ttc tat ccc agc gac Phe Tyr Pro Ser Asp 375	o Ile Ala Val Glu Tr	o Glu
	gag aac aac tac aag Glu Asn Asn Tyr Lys 390		
	ttc ttc ctc tac ago Phe Phe Leu Tyr Ser 405		_
	ggg aac gtc ttc tca Gly Asn Val Phe Ser 420		
	tac acg cag aag agc Tyr Thr Gln Lys Ser 435	<u> </u>	
aaa tga Lys			1398

<210> 19 <211> 465 <212> PRT

<213> Homo Sapiens

<400> 19

Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser
-15 -10 -5

Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
-1 1 5 10

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe 15 20 25

Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu 30 40 45

Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly 50 55 60

Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser 65 70 75

Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr 80 85 90

Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly 95 100 105

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe 110 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu 160 165 170

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser 175 180 185

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro 190 195 200 205

Ser	Asn	Thr	Lys	Val 210	Asp	Lys	Arg	Val	Glu 215	Pro	Lys	Ser	Cys	Asp 220	Lys
Thr	His	Thr	Cys 225	Pro	Pro	Cys	Pro	Ala 230	Pro	Glu	Leu	Leu	Gly 235	Gly	Pro
Ser	Val	Phe 240	Leu	Phe	Pro	Pro	Lys 245	Pro	Lys	Asp	Thr	Leu 250	Met	Ile	Ser
Arg	Thr 255	Pro	Glu	Val	Thr	Cys 260	Val	Val	Val	Asp	Val 265	Ser	His	Glu	Asp
Pro 270	Glu	Val	Lys	Phe	Asn 275	Trp	Tyr	Val	Asp	Gly 280	Val	Glu	Val	His	Asn 285
Ala	Lys	Thr	Lys	Pro 290	Arg	Glu	Glu	Gln	Tyr 295	Asn	Ser	Thr	Tyr	Arg 300	Val
Val	Ser	Val	Leu 305	Thr	Val	Leu	His	Gln 310	Asp	Trp	Leu	Asn	Gly 315	Lys	Glu
Tyr	Lys	Cys 320	Lys	Val	Ser	Asn	Lys 325	Ala	Leu	Pro	Ala	Pro 330	Ile	Glu	Lys
Thr	Ile 335	Ser	Lys	Ala	Lys	Gly 340	Gln	Pro	Arg	Glu	Pro 345	Gln	Val	Tyr	Thr
Leu 350	Pro	Pro	Ser	Arg	Asp 355	Glu	Leu	Thr	Lys	Asn 360	Gln	Val	Ser	Leu	Thr 365
Cys	Leu	Val	Lys	Gly 370	Phe	Tyr	Pro	Ser	Asp 375	Ile	Ala	Val	Glu	Trp 380	Glu
Ser	Asn	Gly	Gln 385	Pro	Glu	Asn	Asn	Tyr 390	Lys	Thr	Thr	Pro	Pro 395	Val	Leu
Asp	Ser	Asp 400	Gly	Ser	Phe	Phe	Leu 405	Tyr	Ser	Lys	Leu	Thr 410	Val	Asp	Lys

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu

ser	415	Trp	GIN	GIN	GIA	420	vai	Pne	Ser	Cys	Ser 425	Val	Met	His	Glu	
Ala 430		His	Asn	His	Tyr 435	Thr	Gln	Lys _.	Ser	Leu 440	Ser	Leu	Ser	Pro	Gly 445	
Lys																
<21 <21 <21 <21	1> : 2> :	20 1398 DNA Homo	Sap	iens												
<22 <22 <22	1> ı	misc Low			te R:	isk I	Humai	n Eng	gine	ered	ING	-1 H	eavy	Cha	in (HC)	
<22 <22 <22	1> (CDS (1).	. (13	95)												
<22 <22 <22	1> r	mat_] (58)	_	ide												
	gct												gcc Ala			48
				atc					tct				gtg Val	aag		96
cct Pro	gga Gly 15	gag Glu	tca Ser	gtc Val	aag Lys	atc Ile 20	tcc Ser	tgc Cys	aag Lys	gct Ala	tct Ser 25	gga Gly	tat Tyr	acc Thr	ttc Phe	144
													caa Gln			192
													aca Thr			240
													tct Ser 75			288

						tct Ser										336
						ggc Gly 100										384
						tca Ser							_	-		432
						aag Lys										480
						tac Tyr			Glu							528
						agc Ser										576
						tcc Ser 180				-						624
						acc Thr								_		672
_			-		_	aag Lys	_	-					_	_		720
						tgc Cys						-	-		-	768
	-					cca Pro			_	_			_			816
						tgc Cys 260										864
						tgg Trp										912
gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgg	gtg	960

Ala	Lys	Thr	Lys	Pro 290	Arg	Glu	Glu	Gln	Tyr 295	Asn	Ser	Thr	Tyr	Arg 300	Val	
												aat Asn				1008
												ccc Pro 330				1056
												cag Gln				1104
												gtc Val				1152
												gtg Val				1200
												cct Pro			_	1248
												acc Thr 410				1296
												gtg Val				1344
												ctg Leu				1392
aaa Lys	tga															1398

<210> 21

<211> 465

<212> PRT

<213> Homo Sapiens

<400> 21

Met Ala Trp Val Ser Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser -15 -10 -5

Ala Gl
n Ala Gl
n Ile Gl
n Leu Val Gl
n Ser Gly Ala Glu Val Lys Lys $-1 \quad 1 \quad \qquad 5 \quad \qquad 10$

Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe 15 20 25

Thr Lys Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 30 35 40 45

Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
50 55 60

Gln Lys Phe Gln Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser 65 70 75

Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 80 85 90

Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly 95 100 105

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe 110 125 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp 145 150 155

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu 160 165 170

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser 175 180 185

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro 190 195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu

```
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 430
                     435
                                         440
 Lys
 <210> 22
 <211> 91
 <212> DNA
 <213> HomoSapiens
 <220>
 <221> misc_feature
 <223>
        GL1 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
        (gamma low)
 <400> 22
 tgtcgacacc atggcttggg tgtccacctt gctattcctg atggcagctg cccaaagtgc
                                                                       60
 ccaagcacag atccagttgg tgcagtctgg a
                                                                       91
 <210> 23
..<211> 90
 <212>
        DNA
 <213> HomoSapiens
 <220>
 <221>
        misc_feature
 <223>
        GL2 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
        (gamma low)
 <400> 23
 atattttgtg aaggtatatc cagaagcctt gcaggagatc ttgacggact ctccaggctt
                                                                       60
 cttcacctca ggtccagact gcaccaactg
                                                                       90
 <210>
        24
 <211> 91
 <212> DNA
 <213> HomoSapiens
 <220>
 <221>
        misc_feature
 <223>
        GL3 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
        (gamma low)
```

tggatatacc ttcacaaaat atggaatgaa ctgggtgaag caggctccag gacagggttt	60
aaagtggatg ggctggataa acacctacac t	91
<210> 25 <211> 90 <212> DNA <213> HomoSapiens	
<220> <221> misc_feature <223> GL4 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)	3
<400> 25 cagtgctagt agaggtgtcc aaggtgaagg taaaccgtcc cttgaagtca tcaccatatg	60
ttggctcttc agtgtaggtg tttatccagc	90
<210> 26 <211> 90 <212> DNA <213> HomoSapiens	
<220> <221> misc_feature <223> GL5 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligo (gamma low)	os
<400> 26	
gacacctcta ctagcactgc ctatttggaa atctcttctc tccggagtga ggacacggct	60
acatatttct gtgcaagatt tggctctgct	90
<210> 27 <211> 85 <212> DNA <213> HomoSapiens	
<220> <221> misc_feature <223> GL6 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos (gamma low)	
<400> 27 gaccgatggg ccctttgtgc tggctgagga gacggtgacc aaggttcctt gaccccagta	60

gtccac	agca gagccaaatc ttgca	85
<210><211><211><212><213>		
<220> <221> <223>	misc_feature Human Engineered ING-1 Heavy Chain Oligos-Low Risk Primers Forward primer:GF	
<400>	28	
ttatgt	cgac accatggctt gg	22
<210><211><211><212><213>	29 17 DNA HomoSapiens	
<220> <221> <223>	misc_feature Human Engineered ING-1 Heavy Chain Oligos Low Risk Primers -Reverse Primer GR	
<220> <221> <223>	misc_feature ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR	
<400>	29	
gaccgat	tggg ccctttg	17
<210><211><211><212><213>	90	
<220> <221> <223>	misc_feature GM2 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-L + Moderate Risk Primers	ow
<400>	30	
atattt	tgtg aaggtatatc cagaagcctt gcaggagatc ttgactgact ctccaggctt	60
cttcacc	ctca gctccagact gcaccaactg	90

```
<210> 31
<211>
      91
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
<223> GM3 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
       + Moderate Risk Primers
<400> 31
tggatatacc ttcacaaaat atggaatgaa ctgggtgcga caggctccag gacaaggttt
                                                                     60
agagtggatg ggctggataa acacctacac t
                                                                     91
<210> 32
<211> 90
<212> DNA
<213> HomoSapiens
<220>
<221> misc feature
<223> GM4 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
       + Moderate Risk Primers
<400> 32
cagtgctagt agaggtgtcc aaggtgaagg taaaccgtcc ctggaacttc tgaccatatg
                                                                      60
                                                                     90
ttggctcttc agtgtaggtg tttatccagc
<210> 33
<211> 90
<212> DNA
<213> HomoSapiens
<220>
<221> misc_feature
      GM5 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
       + Moderate Risk Primers
<400> 33
gacacctcta ctagcactgc ctatttggaa atctcttcgc tccggagtga ggacacggct
                                                                     60
gtgtatttct gtgcaagatt tggctctgct
                                                                     90
<210> 34
<211> 720
<212> DNA
```

<213> Homo sapiens <220> <221> misc feature <223> P1=P Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) <220> <221> CDS <222> (1)..(717)<220> <221> mat_peptide <222> (61)..()<400> 34 atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgq atc cct 48 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro -15 -10 gga tee act gca gac ate gtg atg acc cag tet eca ete tee aat eca 96 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro -1 1 gtc act ctg gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt 144 Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser 20 ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa 192 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys 35 cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga qcc 240 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala 45 50 tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc 288 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe 65 act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac 336 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr 80 tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag 384 Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys 100 ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg 432 Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro 110 cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg 480

Pro Ser Asy 125	Glu (Gln Leu 130		Ser	Gly	Thr	Ala 135	Ser	Val	Val	Суs	Leu 140	
ctg aat aad Leu Asn Asi	n Phe 7												528
aac gcc cto Asn Ala Le													576
agc aag gad Ser Lys Asj 179	Ser 1												624
gca gac tac Ala Asp Ty: 190													672
ggc ctg ago Gly Leu Se: 205			Thr									tag	720
<210> 35 <211> 239													
<212> PRT <213> Homo	sapie	ens											
	sapie	ens											
<213> Homo	-			Leu	Gly	Leu	Leu -10	Val	Leu	Trp	Ile	Pro -5	
<213> Home <400> 35 Met Arg Phe	· Ser Æ	Ala Glr -15 Asp Ile					-10					- 5	
<213> Homo <400> 35 Met Arg Pho -20	Ser # - Ala # -1 1	Ala Glr -15 Asp Ile 1	Val	Met	Thr 5	Gln	-10 Ser	Pro	Leu	Ser 10	Asn	-5 Pro	
<213> Home <400> 35 Met Arg Phe -20 Gly Ser Thi Val Thr Lev	e Ser A	Ala Glr -15 Asp Ile 1	Val	Met Ser 20	Thr 5	Gln Ser	-10 Ser Cys	Pro Arg	Leu Ser 25	Ser 10	Asn Lys	-5 Pro Ser	
<213> Home <400> 35 Met Arg Phe -20 Gly Ser The Val Thr Leg 15 Leu Leu His	Ser A	Ala Glr -15 Asp Ile 1 Glu Ser Asn Gly	Val Gly Ile 35	Met Ser 20	Thr 5 Ile Tyr	Gln Ser Leu	-10 Ser Cys	Pro Arg Trp 40	Leu Ser 25 Tyr	Ser 10 Ser	Asn Lys Gln	-5 Pro Ser Lys	

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys 95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro 110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu 125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp 145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp 160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys 175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 190 195 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 205 210 215

<210> 36

<211> 720

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> P2=P Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 15 (P2)

<220>

<221> CDS

<222> (1)..(717)

<220>

<221> mat_peptide

<222> (61)..()

<400)> 3	36															
													tgg Trp			48	
													tcc Ser 10			96	
													agt Ser			144	
													ctg Leu			192	
													aac Asn			240	
													aca Thr			288	
													gtt Val 90			336	
													ggc Gly			384	
							_	_			_		atc Ile		_	432	
													gtg Val			480	
ctg Leu	aat Asn	aac Asn	ttc Phe	tat Tyr 145	ccc Pro	aga Arg	gag Glu	gcc Ala	aaa Lys 150	gta Val	cag Gln	tgg Trp	aag Lys	gtg Val 155	gat Asp	528	
aac Asn	gcc Ala	ctc Leu	caa Gln 160	tcg Ser	ggt Gly	aac Asn	tcc Ser	cag Gln 165	gag Glu	agt Ser	gtc Val	aca Thr	gag Glu 170	cag Gln	gac Asp	576	
											_	_	ctg Leu	_		624	

gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 195 ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 720 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 210 215 <210> 37 <211> 239 <212> PRT <213> Homo sapiens <400> 37 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro -20 -15 -10 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro -1 1 Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser . 15 20 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Ser Gly Ser Gly Thr Asp Phe 65 70 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr 80 85 Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys 95 100 105 Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro

120

115

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu

110

125 130 135 140 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp 160 165 170 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys 175 180 185 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 190 195 200 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 205 210 <210> 38 <211> 720 <212> DNA <213> Homo sapiens <220> <221> misc_feature <223> P3=P Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 18 (P3) <220> <221> CDS <222> (1)..(717) <220> <221> mat_peptide <222> (61)..() atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct 48 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro -20 -15 -10 gga tee act gea gae ate gtg atg acc eag tet gea ete tee aat eea 96 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro -1 1 gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aaq aqt 144 Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser 15 20 25

			atc Ile 35		_			-	_		192
			ctg Leu								240
			ttc Phe								288
			gtg Val								336
			ctt Leu								384
			gtg Val 115								432
			aaa Lys			_	-		_	-	480
			aga Arg							_	528
			aac Asn						_	_	576
			agc Ser								624
			aaa Lys 195								672
			aca Thr							tag	720

<210> 39 <211> 239

<212> PRT

<213> Homo sapiens

<400> 39

Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro -20 -15 -10 -5

Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro $-1 \ 1 \ 5 \ 10$

Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser 15 20 25

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys 30 40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala 45 50 55 60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe 65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr 80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys 95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro 110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu 125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp 145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp 160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys 175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 190 195 200
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 205 210 215
<210> 40 <211> 720 <212> DNA <213> Homo sapiens
<220> <221> misc_feature <223> P1P2=Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 15(P2)
<220> <221> CDS <222> (1)(717)
<220> <221> mat_peptide <222> (61)()
<pre><400> 40 atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct 48 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro -20 -15 -10 -5</pre>
gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro -1 1 5 10
gtc act cct gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser 15 20 25
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa 192 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys 30 35 40
cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala 50 55 60
tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe 65 70 75

Thr	Leu	Lys	Ile 80	Ser	Arg	Val	Glu	Ala 85	Glu	Asp	Val	Gly	Val 90	Tyr	Tyr	
														acc Thr		384
											_			ttc Phe	_	432
														tgc Cys		480
														gtg Val 155		528
														cag Gln		576
											_	_	_	agc Ser		624
									-	_	_	-		cat His	_	672
	ctg Leu													tgt Cys	tag	720
<210 <211 <212 <213	l> 2 2> I	11 239 PRT Homo	sapi	iens												
<400)> 4	11														
Met -20	Arg	Phe	Ser	Ala	Gln -15	Leu	Leu	Gly	Leu	Leu -10	Val	Leu	Trp	Ile	Pro -5	
Gly	Ser	Thr	Ala -1	Asp 1	Ile	Val	Met	Thr 5	Gln	Ser	Pro	Leu	Ser 10	Asn	Pro	
Val	Thr	Pro 15	Gly	Glu	Ser	Gly	Ser 20	Ile	Ser	Cys	Arg	Ser 25	Ser	Lys	Ser	

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys 30 35 40

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala 45 50 55 60

Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe 65 70 75

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr 80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys 95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro 110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu 125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp 145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp 160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys 175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 190 195 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 205 210 215

<210> 42

<211> 720

<212> DNA

<213> Homo sapiens

```
<220>
<221>
      misc_feature
<223>
       P1P3 = Human Engineered (low risk) ING1 light Chain with one
       moderate risk proline change; proline at position 8 (P1) 18 (P3)
<220>
<221>
       CDS
<222>
       (1)..(717)
<220>
<221>
      mat_peptide
<222>
       (61)..()
<400> 42
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct
                                                                       48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
                    -15
                                        -10
gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca
                                                                       96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
            -1
gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt
                                                                      144
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
                            20
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa
                                                                      192
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
    30
                        35
cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc
                                                                      240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
                    50
tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc
                                                                      288
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
                65
act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac
                                                                      336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag
                                                                      384
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
                            100
ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg
                                                                      432
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    110
                        115
cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg
                                                                      480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
125
                    130
                                        135
                                                             140
```

	aat Asn															528
	gcc Ala															576
	aag Lys															624
	gac Asp 190															672
	ctg Leu														tag	720
<210 <210 <210 <210	1> 2 2> 1	43 239 PRT Homo	sap	iens												
<400	O> 4	43									•					
)> 4 Arg		Ser	Ala	Gln -15	Leu	Leu	Gly	Leu	Leu -10	Val	Leu	Trp	Ile	Pro -5	
Met -20		Phe			-15					-10					-5	·
Met -20	Arg	Phe	Ala -1	Asp 1	-15	Val	Met	Thr 5	Gln	-10 Ser	Pro	Leu	Ser 10	Asn	-5 Pro	
Met -20 Gly Val	Arg Ser	Phe Thr Leu 15	Ala -1 Gly	Asp 1 Glu	-15 Ile Pro	Val Gly	Met Ser 20	Thr 5	Gln Ser	-10 Ser Cys	Pro Arg	Leu Ser 25	Ser 10 Ser	Asn Lys	-5 Pro Ser	
Met -20 Gly Val	Arg Ser Thr	Phe Thr Leu 15	Ala -1 Gly Ser	Asp 1 Glu Asn	-15 Ile Pro Gly	Val Gly Ile 35	Met Ser 20	Thr 5 Ile Tyr	Gln Ser Leu	-10 Ser Cys	Pro Arg Trp 40	Leu Ser 25 Tyr	Ser 10 Ser Leu	Asn Lys Gln	-5 Pro Ser Lys	

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr

80 85 90

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys 95 100 105

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro 110 115 120

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu 125 130 135 140

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp 145 150 155

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp 160 165 170

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys 175 180 185

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 190 200

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 205 210 215

<210> 44

<211> 720

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> P2P3=Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 8 (P1) 18 (P3)

<220>

<221> CDS

<222> (1)..(717)

<220>

<221> mat_peptide

<222> (61)..()

<400)> 4	14														
atg	agg						ctg Leu				_					48
							atg Met									96
_				_	_		tcc Ser 20			_			_	_	_	144
							act Thr		-				-	_		192
							ctc Leu									240
							agt Ser									288
							gag Glu									336
							ccg Pro 100								-	384
							gct Ala				-				_	432
		_		_	_		tct Ser			_		_		_	_	480
							gag Glu									528
							tcc Ser			-	_			_	_	576
							ctc Leu 180	-	-		_	_	_	_		624
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	672

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 190 195 ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 720 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 205 210 215 <210> 45 <211> 239 <212> PRT <213> Homo sapiens <400> 45 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro -10 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro -1 1 Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser 15 20 25 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys 30 35 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala 50 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe 65 70 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr 80 85

Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys

Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu

120

140

135

100

115

130

95

110

125

Leu	Asn	Asn	Phe	Туг 145	Pro	Arg	Glu	Ala	Lys 150	Val	Gln	Trp	Lys	Val 155	Asp	
Asn	Ala	Leu	Gln 160	Ser	Gly	Asn	Ser	Gln 165	Glu	Ser	Val	Thr	Glu 170	Gln	Asp	
Ser	Lys	Asp 175	Ser	Thr	Tyr	Ser	Leu 180	Ser	Ser	Thr	Leu	Thr 185	Leu	Ser	Lys	
Ala	Asp 190	Tyr	Glu	Lys	His	Lys 195	Val	Tyr	Ala	Cys	Glu 200	Val	Thr	His	Gln	
Gly 205	Leu	Ser	Ser	Pro	Val 210	Thr	Lys	Ser	Phe	Asn 215	Arg	Gly	Glu	Cys		
<210 <211 <212 <213 <220 <220	L>	46 85 DNA Homo misc_														
<223)> 4	P1 01 46														
acto	ttad	cta g	gacco	gcag	gg ag	gatgo	gaaco	tga	actct	CCC	agag	gtgad	etg g	gatto	gagag	60
tgga	agact	tgg g	gtcat	cacg	ja to	ıtct										85
<210 <211 <212 <213	-> { ?> I	47 85 ONA Homo	Sapi	ens												
	.> r	misc_ P2 Ol			ın Er	ngine	ered	l ING	5-1 w	rith	prol	ine	olig	ios		
<400 acto		17 cta g	jaccg	ıgcaç	g ag	ratgo	jaacc	: tga	ıctct	cca	ggag	ıtgac	tg g	gatto	ıgagag	60
tgca	ıgact	gg g	tcat	cacg	ga tg	tct										85

<210> 48

<211> <212>	85 DNA	
<213>	Homo Sapiens	
<220>		
<221> <223>	<pre>misc_feature P3 Oligo Human Engineered ING-1 with proline oligos</pre>	
<400>	48	
actetta	acta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag	60
tgcagad	etgg gtcatcacga tgtct	85
<210>	49	
<211>	85	
<212>	DNA	
<213>	Homo Sapiens	
<220>		
<221>	misc_feature	
<223>	P1P2 Oligo Human Engineered ING-1 with proline oligos	
<400>	49	
actctta	acta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag	60
tgcagad	etgg gtcatcacga tgtct	85
<210>	50	
<211>	85	
<212>	DNA	
<213>	Homo Sapiens	
<220>		
<221>	misc_feature	
<223>	P1P3 Oligo Human Engineered ING-1 with proline oligos	
<400>		
actctta	acta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag	60
tggagad	tgg gtcatcacga tgtct	85
<210>	51	
<211>	85	
<212>	DNA	
<213>	Homo Sapiens	

<220>

<221> <223>		_		uman	Eng	ineer	red I	ING-1	l wit	th pi	roli	ne ol	ligo:	5	
<400>	51														
actctt	acta	gacc	ggca	gg ag	gatg	gaac	c cgg	gctct	tcca	ggag	gtgad	ctg o	gatt	ggagag	60
tgcaga	ctgg	gtca	tcac	ga to	gtct										85
<210>	52														
<211>	19														
<212> <213>	DNA Homo	Sap	iens												
		-													
<220>															
<221>	misc	_fea	ture												
<223>	Reve	rse :	Prime	er Kl	3sr 3	ING-	l Lig	ght (Chair	n					
<400>	52														
cttact		cggc	agga	g											19
<210>	53														
<211>	798														
<212>															
<213>	Homo	sap:	ıens												
<220>		_													
<221> <223>	misc	_feat m tr		ted (comi	anco									
\ZZ 3>	Брса	III CI	unca	ceu .	seque	siice									
<220>															
<221> <222>	CDS	(79	5)												
1222	(- / •	. (7)	<i>J</i> ,												
<400>	53														
atg gc Met Al															48
1	2 110	110	5	V 0 1	Deu	711u	1110	10	пса	Бей	Dea	nia	15	AΙα	
acg gc Thr Al															96
		20				0111	25	O ₂ u	C 10	Vul	Cys	30	******	171	
aag ct Lys Le															144
בי טע	35	vai	71511	Cys	THE	40	NSII	non	NJII	Arg	45	Суз	GIII	Cys	
act tc Thr Se															192
50	. val	GIĀ	AIG	GIII	55	TIIL	vaı	тте	cys	60	пÀЯ	ьeu	AId	нта	
										-					

			gca Ala						2	40
			gcc Ala						2	88
			ggg Gly						3	36
			gtg Val						3	84
			tgc Cys 135						4	32
			aaa Lys						4	80
			cag Gln						5	28
	•		agt Ser						5	76
			tct Ser			_	_	 	6	24
			tat Tyr 215						6	72
			atg Met						7:	20
			act Thr				-	-	7	68
			ggt Gly		taa				7:	98

<211> 265

<212> PRT

<213> Homo sapiens

<400> 54

Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala 1 5 10 15

Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr 20 25 30

Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys 35 40 45

Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala 50 55 60

Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg 70 75 80

Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp 85 90 95

Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly 100 105 110

Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp 115 120 125

Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile 130 135 140

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu 165 170 175

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr 180 185 190

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys T 195 200	Thr Gln Asn Asp Val Asp 205
Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys A 210 215	asp Val Lys Gly Glu Ser 220
Leu Phe His Ser Lys Lys Met Asp Leu Thr V 225 230 2	Val Asn Gly Glu Gln Leu 235 240
Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr T 245 250	Tyr Val Asp Glu Lys Ala 255
Pro Glu Phe Ser Met Gln Gly Leu Lys 260 265	
<210> 55 <211> 945 <212> DNA <213> Homo sapiens	
<220> <221> misc_feature <223> Full-Length EpCam	
<220> <221> CDS <222> (1)(942)	
<220> <221> mat_peptide <222> (70)()	
<pre><400> 55 atg gcg ccc ccg cag gtc ctc gcg ttc ggg c Met Ala Pro Pro Gln Val Leu Ala Phe Gly L -20 -15</pre>	
acg gcg act ttt gcc gca gct cag gaa gaa t Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu C -5 -1 1	
aag ctg gcc gta aac tgc ttt gtg aat aat a Lys Leu Ala Val Asn Cys Phe Val Asn Asn A 10 15 2	
act tca gtt ggt gca caa aat act gtc att t Thr Ser Val Gly Ala Gln Asn Thr Val Ile C 30 35	

						gca Ala										240
						gcc Ala									-	288
						80 Gly ggg										336
						gtg Val			-		_	_	_			384
						tgc Cys										432
						aaa Lys								-		480
						cag Gln									-	528
						agt Ser 160							_			576
	_	_	_			tct Ser					_		_		_	624
						tat Tyr										672
						atg Met										720
						act Thr										768
						ggt Gly 240			-		_			_		816
gtg	gtt	gtg	gtg	ata	gca	gtt	gtt	gct	gga	att	gtt	gtg	ctg	gtt	att	864

Val 250	Val	Val	Val	Ile	Ala 255	Val	Val	Ala	Gly	Ile 260	Val	Val	Leu	Val	Ile 265	
						gca Ala										912
						gaa Glu				taa						945
<210 <210 <210 <210	l> 3 2> 1	56 314 PRT Homo	sap:	iens												
<400)> !	56											•			
Met	Ala	Pro	Pro -20	Gln	Val	Leu	Ala	Phe -15	Gly	Leu	Leu	Leu	Ala -10	Ala	Ala	
Thr	Ala	Thr -5	Phe	Ala	Ala	Ala -1	Gln 1	Glu	Glu	Cys	Val 5	Cys	Glu	Asn	Tyr	
Lys 10	Leu	Ala	Val	Asn	Cys 15	Phe	Val	Asn	Asn	Asn 20	Arg	Gln	Суз	Gln	Cys 25	
Thr	Ser	Val	Gly	Ala 30	Gln	Asn	Thr	Val	Ile 35	Суз	Ser	Lys	Leu	Ala 40	Ala	
Lys	Cys	Leu	Val 45	Met	Lys	Ala	Glu	Met 50	Asn	Gly	Ser	Lys	Leu 55	Gly	Arg	
Arg	Ala	Lys 60	Pro	Glu	Gly	Ala	Leu 65	Gln	Asn	Asn	Asp	Gly 70	Leu	Tyr	Asp	
Pro	Asp 75	Cys	Asp	Glu	Ser	Gly 80	Leu	Phe	Lys	Ala	Lys 85	Gln	Cys	Asn	Gly	
Thr 90	Ser	Thr	Cys	Trp	Cys 95	Val	Asn	Thr	Ala	Gly 100	Val	Arg	Arg	Thr	Asp 105	
Lys	Asp	Thr	Glu	Ile 110	Thr	Суѕ	Ser	Glu	Arg 115	Val	Arg	Thr	Tyr	Trp 120	Ile	

Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys 125 130 135

Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu 140 145 150

Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr 155 160 165

Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp 170 185

Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser 190 195 200

Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu 205 210 215

Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala 220 225 230

Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile 235 240 245

Val Val Val Ile Ala Val Val Ala Gly Ile Val Val Leu Val Ile 250 255 260 265

Ser Arg Lys Lys Arg Met Ala Lys Tyr Glu Lys Ala Glu Ile Lys Glu 270 275 280

Met Gly Glu Met His Arg Glu Leu Asn Ala 285 290

<210> 57

<211> 26

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Forward Primer (for both soluble and full length Ep-CAM): EC-1

```
<400> 57
ttatgtcgac agcatggcgc ccccgc
                                                                   26
<210> 58
<211> 31
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Ep-CAM Reverse Primer (for soluble Ep-CAM): EC-2
<400> 58
gagttacgtc ccagatttta ttgggccccc t
                                                                   31
<210> 59
<211> 30
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<223> Ep-CAM Reverse Primer (for full-length Ep-CAM): EC-3
<400> 59
                                                                   30
gtatcccttg agttacgtat tgagctcgtt
```